

RAW SEQUENCE LISTING

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Application Serial Number: 08/989,896
Source: IFWO
Date Processed by STIC: 09-12-2005

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RAW SEQUENCE LISTING

DATE: 09/12/2005

PATENT APPLICATION: US/08/989,896

TIME: 12:57:56

Input Set : N:\Cr3\RULE60\08989896.raw.txt

Output Set: N:\CRF4\09092005\H989896.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Gehrman, Mathias
6                Seemann, Gerhard
7                Bosslet, Klaus
8                Czech, Joerg
10    (ii) TITLE OF INVENTION: Fusion Protein for Prodrug Activity
12    (iii) NUMBER OF SEQUENCES: 18
14    (iv) CORRESPONDENCE ADDRESS:
15         (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
16                Dunner
17         (B) STREET: 1300 I Street, N.W.
18         (C) CITY: Washington
19         (D) STATE: D.C.
20         (E) COUNTRY: USA
21         (F) ZIP: 20005-3315
23    (v) COMPUTER READABLE FORM:
24         (A) MEDIUM TYPE: Floppy disk
25         (B) COMPUTER: IBM PC compatible
26         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27         (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29    (vi) CURRENT APPLICATION DATA:
C--> 30         (A) APPLICATION NUMBER: US/08/989,896
C--> 31         (B) FILING DATE: 12-Dec-1997
33    (vii) PRIOR APPLICATION DATA:
W--> 34         (A) APPLICATION NUMBER: US/08/475,826
35         (B) FILING DATE: 07-JUN-1995
W--> 36         (A) APPLICATION NUMBER: US 08/129,379
37         (B) FILING DATE: 30-SEP-1993
W--> 39         (A) APPLICATION NUMBER: DE P 42 33 152.8
40         (B) FILING DATE: 02-OCT-1992
42    (viii) ATTORNEY/AGENT INFORMATION:
43         (A) NAME: Barker, M. P.
44         (B) REGISTRATION NUMBER: 32,013
45         (C) REFERENCE/DOCKET NUMBER: 02481.1337-00000
47    (ix) TELECOMMUNICATION INFORMATION:
48         (A) TELEPHONE: 202-408-4000
49         (B) TELEFAX: 202-408-4400
52 (2) INFORMATION FOR SEQ ID NO: 1:
54     (i) SEQUENCE CHARACTERISTICS:
55         (A) LENGTH: 3314 base pairs
56         (B) TYPE: nucleic acid
57         (C) STRANDEDNESS: single

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58      (D) TOPOLOGY: linear
60      (ii) MOLECULE TYPE: DNA (genomic)
63      (ix) FEATURE:
64          (A) NAME/KEY: sig_peptide
65          (B) LOCATION: 145..283
67      (ix) FEATURE:
68          (A) NAME/KEY: mat_peptide
69          (B) LOCATION: join(284..1003, 1069..1119, 1263..3161)
71      (ix) FEATURE:
72          (A) NAME/KEY: CDS
73          (B) LOCATION: join(145..189, 272..1003, 1069..1119, 1263..3161)
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78 CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA ATCTACATGG      60
80 TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA GATCACAGTT CTCTCTACAG      120
82 TTACTGAGCA CACAGGACCT CACC ATG GGA TGG AGC TGT ATC ATC CTC TTC      171
83                                     Met Gly Trp Ser Cys Ile Ile Leu Phe
84                                     -19                      -15
86 TTG GTA GCA ACA GCT ACA GGTAAGGGGC TCACAGTAGC AGGCTTGAGG      219
87 Leu Val Ala Thr Ala Thr
88 -10                      -5
90 TCTGGACATA TATATGGGTG ACAATGACAT CCACTTTGCC TTTCTCTCCA CA GGT      274
91                                     Gly
92                                     -4
94 GTC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA      322
95 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
96          1          5          10
98 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC ACC ATC      370
99 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile
100      15          20          25
102 AGC AGT GGT TAT AGC TGG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT      418
103 Ser Ser Ser Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly
104 30          35          40          45
106 CTT GAG TGG ATT GGA TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC      466
107 Leu Glu Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn
108          50          55          60
110 CCC TCT CTC AAA AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC      514
111 Pro Ser Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
112          65          70          75
114 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC      562
115 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
116          80          85          90
118 TAT TAT TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC      610
119 Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val
120          95          100          105
122 TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG      658
123 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
124 110          115          120          125
126 GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC CAG      706
127 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln

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128	130	135	140	
130 AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC				754
131 Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr				
132	145	150	155	
134 TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC CAG CAG AAG				802
135 Cys Ser Thr Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys				
136	160	165	170	
138 CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA TCC AAC CTG GCT				850
139 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala				
140	175	180	185	
142 TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC				898
143 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe				
144 190	195	200	205	
146 ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC				946
147 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr				
148	210	215	220	
150 TGC CAT CAG TGG AGT AGT TAT CCC ACG TTC GGC CAA GGG ACC AAG CTG				994
151 Cys His Gln Trp Ser Ser Tyr Pro Thr Phe Gly Gln Gly Thr Lys Leu				
152	225	230	235	
154 GAG ATC AAA GGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTGGATCTG				1043
155 Glu Ile Lys				
156	240			
158 AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA ACC CCA CTT GGT GAC ACA				1095
159		Glu Leu Lys Thr	Pro Leu Gly Asp Thr	
160			245	
162 ACT CAC ACA TGC CCA CGG TGC CCA GGTAAGCCAG CCCAGGACTC GCCCTCCAGC				1149
163 Thr His Thr Cys Pro Arg Cys Pro				
164 250	255			
166 TCAAGGCGGG ACAAGAGCCC TAGAGTGGCC TGAGTCCAGG GACAGGCCCC AGCAGGGTGC				1209
168 TGACGCATCC ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG				1265
169			Ala	
172 GCG GCG GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG				1313
173 Ala Ala Ala Val Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser				
174	260	265	270	
176 CGG GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC				1361
177 Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe				
178 275	280	285	290	
180 TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG CCG				1409
181 Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg Pro				
182	295	300	305	
184 CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC AGC TTC				1457
185 Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser Ser Phe				
186	310	315	320	
188 AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC GGC TGG GTG				1505
189 Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val Gly Trp Val				
190	325	330	335	
192 TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG ACC CAG GAC CTG				1553
193 Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr Gln Asp Leu				
194	340	345	350	

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196	CGC	ACA	AGA	GTG	GTG	CTG	AGG	ATT	GGC	AGT	GCC	CAT	TCC	TAT	GCC	ATC	1601
197	Arg	Thr	Arg	Val	Val	Leu	Arg	Ile	Gly	Ser	Ala	His	Ser	Tyr	Ala	Ile	
198	355					360					365					370	
200	GTG	TGG	GTG	AAT	GGG	GTC	GAC	ACG	CTA	GAG	CAT	GAG	GGG	GGC	TAC	CTC	1649
201	Val	Trp	Val	Asn	Gly	Val	Asp	Thr	Leu	Glu	His	Glu	Gly	Gly	Tyr	Leu	
202					375					380						385	
204	CCC	TTC	GAG	GCC	GAC	ATC	AGC	AAC	CTG	GTC	CAG	GTG	GGG	CCC	CTG	CCC	1697
205	Pro	Phe	Glu	Ala	Asp	Ile	Ser	Asn	Leu	Val	Gln	Val	Gly	Pro	Leu	Pro	
206					390					395					400		
208	TCC	CGG	CTC	CGA	ATC	ACT	ATC	GCC	ATC	AAC	AAC	ACA	CTC	ACC	CCC	ACC	1745
209	Ser	Arg	Leu	Arg	Ile	Thr	Ile	Ala	Ile	Asn	Asn	Thr	Leu	Thr	Pro	Thr	
210			405					410					415				
212	ACC	CTG	CCA	CCA	GGG	ACC	ATC	CAA	TAC	CTG	ACT	GAC	ACC	TCC	AAG	TAT	1793
213	Thr	Leu	Pro	Pro	Gly	Thr	Ile	Gln	Tyr	Leu	Thr	Asp	Thr	Ser	Lys	Tyr	
214		420					425						430				
216	CCC	AAG	GGT	TAC	TTT	GTC	CAG	AAC	ACA	TAT	TTT	GAC	TTT	TTC	AAC	TAC	1841
217	Pro	Lys	Gly	Tyr	Phe	Val	Gln	Asn	Thr	Tyr	Phe	Asp	Phe	Phe	Asn	Tyr	
218	435					440					445					450	
220	GCT	GGA	CTG	CAG	CGG	TCT	GTA	CTT	CTG	TAC	ACG	ACA	CCC	ACC	ACC	TAC	1889
221	Ala	Gly	Leu	Gln	Arg	Ser	Val	Leu	Leu	Tyr	Thr	Thr	Pro	Thr	Thr	Tyr	
222					455					460						465	
224	ATC	GAT	GAC	ATC	ACC	GTC	ACC	ACC	AGC	GTG	GAG	CAA	GAC	AGT	GGG	CTG	1937
225	Ile	Asp	Asp	Ile	Thr	Val	Thr	Thr	Ser	Val	Glu	Gln	Asp	Ser	Gly	Leu	
226					470					475						480	
228	GTG	AAT	TAC	CAG	ATC	TCT	GTC	AAG	GGC	AGT	AAC	CTG	TTC	AAG	TTG	GAA	1985
229	Val	Asn	Tyr	Gln	Ile	Ser	Val	Lys	Gly	Ser	Asn	Leu	Phe	Lys	Leu	Glu	
230			485					490					495				
232	GTG	CGT	CTT	TTG	GAT	GCA	GAA	AAC	AAA	GTC	GTG	GCG	AAT	GGG	ACT	GGG	2033
233	Val	Arg	Leu	Leu	Asp	Ala	Glu	Asn	Lys	Val	Val	Ala	Asn	Gly	Thr	Gly	
234		500					505					510					
236	ACC	CAG	GGC	CAA	CTT	AAG	GTG	CCA	GGT	GTC	AGC	CTC	TGG	TGG	CCG	TAC	2081
237	Thr	Gln	Gly	Gln	Leu	Lys	Val	Pro	Gly	Val	Ser	Leu	Trp	Trp	Pro	Tyr	
238	515					520					525					530	
240	CTG	ATG	CAC	GAA	CGC	CCT	GCC	TAT	CTG	TAT	TCA	TTG	GAG	GTG	CAG	CTG	2129
241	Leu	Met	His	Glu	Arg	Pro	Ala	Tyr	Leu	Tyr	Ser	Leu	Glu	Val	Gln	Leu	
242					535					540						545	
244	ACT	GCA	CAG	ACG	TCA	CTG	GGG	CCT	GTG	TCT	GAC	TTC	TAC	ACA	CTC	CCT	2177
245	Thr	Ala	Gln	Thr	Ser	Leu	Gly	Pro	Val	Ser	Asp	Phe	Tyr	Thr	Leu	Pro	
246					550					555						560	
248	GTG	GGG	ATC	CGC	ACT	GTG	GCT	GTC	ACC	AAG	AGC	CAG	TTC	CTC	ATC	AAT	2225
249	Val	Gly	Ile	Arg	Thr	Val	Ala	Val	Thr	Lys	Ser	Gln	Phe	Leu	Ile	Asn	
250			565					570					575				
252	GGG	AAA	CCT	TTC	TAT	TTC	CAC	GGT	GTC	AAC	AAG	CAT	GAG	GAT	GCG	GAC	2273
253	Gly	Lys	Pro	Phe	Tyr	Phe	His	Gly	Val	Asn	Lys	His	Glu	Asp	Ala	Asp	
254		580					585					590					
256	ATC	CGA	GGG	AAG	GGC	TTC	GAC	TGG	CCG	CTG	CTG	GTG	AAG	GAC	TTC	AAC	2321
257	Ile	Arg	Gly	Lys	Gly	Phe	Asp	Trp	Pro	Leu	Leu	Val	Lys	Asp	Phe	Asn	
258	595					600					605					610	
260	CTG	CTT	CGC	TGG	CTT	GGT	GCC	AAC	GCT	TTC	CGT	ACC	AGC	CAC	TAC	CCC	2369

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261	Leu	Leu	Arg	Trp	Leu	Gly	Ala	Asn	Ala	Phe	Arg	Thr	Ser	His	Tyr	Pro	
262					615					620					625		
264	TAT	GCA	GAG	GAA	GTG	ATG	CAG	ATG	TGT	GAC	CGC	TAT	GGG	ATT	GTG	GTC	2417
265	Tyr	Ala	Glu	Glu	Val	Met	Gln	Met	Cys	Asp	Arg	Tyr	Gly	Ile	Val	Val	
266				630					635					640			
268	ATC	GAT	GAG	TGT	CCC	GGC	GTG	GGC	CTG	GCG	CTG	CCG	CAG	TTC	TTC	AAC	2465
269	Ile	Asp	Glu	Cys	Pro	Gly	Val	Gly	Leu	Ala	Leu	Pro	Gln	Phe	Phe	Asn	
270			645					650					655				
272	AAC	GTT	TCT	CTG	CAT	CAC	CAC	ATG	CAG	GTG	ATG	GAA	GAA	GTG	GTG	CGT	2513
273	Asn	Val	Ser	Leu	His	His	His	Met	Gln	Val	Met	Glu	Glu	Val	Val	Arg	
274		660					665				670						
276	AGG	GAC	AAG	AAC	CAC	CCC	GCG	GTC	GTG	ATG	TGG	TCT	GTG	GCC	AAC	GAG	2561
277	Arg	Asp	Lys	Asn	His	Pro	Ala	Val	Val	Met	Trp	Ser	Val	Ala	Asn	Glu	
278	675					680				685					690		
280	CCT	GCG	TCC	CAC	CTA	GAA	TCT	GCT	GGC	TAC	TAC	TTG	AAG	ATG	GTG	ATC	2609
281	Pro	Ala	Ser	His	Leu	Glu	Ser	Ala	Gly	Tyr	Tyr	Leu	Lys	Met	Val	Ile	
282				695						700					705		
284	GCT	CAC	ACC	AAA	TCC	TTG	GAC	CCC	TCC	CGG	CCT	GTG	ACC	TTT	GTG	AGC	2657
285	Ala	His	Thr	Lys	Ser	Leu	Asp	Pro	Ser	Arg	Pro	Val	Thr	Phe	Val	Ser	
286			710						715				720				
288	AAC	TCT	AAC	TAT	GCA	GCA	GAC	AAG	GGG	GCT	CCG	TAT	GTG	GAT	GTG	ATC	2705
289	Asn	Ser	Asn	Tyr	Ala	Ala	Asp	Lys	Gly	Ala	Pro	Tyr	Val	Asp	Val	Ile	
290			725					730					735				
292	TGT	TTG	AAC	AGC	TAC	TAC	TCT	TGG	TAT	CAC	GAC	TAC	GGG	CAC	CTG	GAG	2753
293	Cys	Leu	Asn	Ser	Tyr	Tyr	Ser	Trp	Tyr	His	Asp	Tyr	Gly	His	Leu	Glu	
294		740					745				750						
296	TTG	ATT	CAG	CTG	CAG	CTG	GCC	ACC	CAG	TTT	GAG	AAC	TGG	TAT	AAG	AAG	2801
297	Leu	Ile	Gln	Leu	Gln	Leu	Ala	Thr	Gln	Phe	Glu	Asn	Trp	Tyr	Lys	Lys	
298	755				760					765					770		
300	TAT	CAG	AAG	CCC	ATT	ATT	CAG	AGC	GAG	TAT	GGA	GCA	GAA	ACG	ATT	GCA	2849
301	Tyr	Gln	Lys	Pro	Ile	Ile	Gln	Ser	Glu	Tyr	Gly	Ala	Glu	Thr	Ile	Ala	
302				775						780					785		
304	GGG	TTT	CAC	CAG	GAT	CCA	CCT	CTG	ATG	TTC	ACT	GAA	GAG	TAC	CAG	AAA	2897
305	Gly	Phe	His	Gln	Asp	Pro	Pro	Leu	Met	Phe	Thr	Glu	Glu	Tyr	Gln	Lys	
306			790					795					800				
308	AGT	CTG	CTA	GAG	CAG	TAC	CAT	CTG	GGT	CTG	GAT	CAA	AAA	CGC	AGA	AAA	2945
309	Ser	Leu	Leu	Glu	Gln	Tyr	His	Leu	Gly	Leu	Asp	Gln	Lys	Arg	Arg	Lys	
310			805					810					815				
312	TAT	GTG	GTT	GGA	GAG	CTC	ATT	TGG	AAT	TTT	GCC	GAT	TTC	ATG	ACT	GAA	2993
313	Tyr	Val	Val	Gly	Glu	Leu	Ile	Trp	Asn	Phe	Ala	Asp	Phe	Met	Thr	Glu	
314		820					825				830						
316	CAG	TCA	CCG	ACG	AGA	GTG	CTG	GGG	ATT	AAA	AAG	GGG	ATC	TTC	ACT	CGG	3041
317	Gln	Ser	Pro	Thr	Arg	Val	Leu	Gly	Asn	Lys	Lys	Gly	Ile	Phe	Thr	Arg	
318	835					840				845					850		
320	CAG	AGA	CAA	CCA	AAA	AGT	GCA	GCG	TTC	CTT	TTG	CGA	GAG	AGA	TAC	TGG	3089
321	Gln	Arg	Gln	Pro	Lys	Ser	Ala	Ala	Phe	Leu	Leu	Arg	Glu	Arg	Tyr	Trp	
322				855					860						865		
324	AAG	ATT	GCC	AAT	GAA	ACC	AGG	TAT	CCC	CAC	TCA	GTA	GCC	AAG	TCA	CAA	3137
325	Lys	Ile	Ala	Asn	Glu	Thr	Arg	Tyr	Pro	His	Ser	Val	Ala	Lys	Ser	Gln	

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:36 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)

L:39 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)